GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 80 Seconds
(without alignments)
742.515 Million cell updates/sec

Title: US-09-824-134-2_COPY_130_245
Perfect score: 593
Sequence: 1 FEAGAAAGAAPGEEDLCAAF.....QEVQQARDLQNRSGAMSPMS 116

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	593	100.0	149	2	Q6LCB0	Q6lcb0 homo sapien
2	593	100.0	208	1	FADD_HUMAN	Q13158 homo sapien
3	389	65.6	209	2	Q645M6	Q645m6 bos taurus
4	382.5	64.5	205	1	FADD_MOUSE	Q61160 mus musculu
5	382.5	64.5	205	2	Q8CD57	Q8cd57 mus musculu
6	381	64.2	208	2	Q8R2E7	Q8r2e7 rattus norv
7	189	31.9	189	2	Q6Q782	Q6q782 ictalurus p
8	115.5	19.5	656	1	RIK1_MOUSE	Q60855 mus musculu
9	114.5	19.3	1719	2	Q13768	Q13768 homo sapien
10	114.5	19.3	1856	2	Q99407	Q99407 homo sapien
11	114.5	19.3	1880	1	ANK1_HUMAN	P16157 homo sapien
12	114	19.2	239	2	Q9V3B4	Q9v3b4 drosophila
13	112.5	19.0	1848	2	Q61302	Q61302 mus musculu
14	112.5	19.0	1862	1	ANK1_MOUSE	Q02357 mus musculu
15	111.5	18.8	671	1	RIK1_HUMAN	Q13546 homo sapien
16	108.5	18.3	663	2	Q7ZZX8	Q7zzx8 gallus gall
17	103.5	17.5	461	2	O96407	O96407 litomosoide
18	103	17.4	970	2	Q17342	Q17342 caenorhabdi
19	103	17.4	985	2	Q17341	Q17341 caenorhabdi
20	103	17.4	1786	2	Q17344	Q17344 caenorhabdi
21	103	17.4	1809	2	Q17487	Q17487 caenorhabdi
22	103	17.4	1815	2	Q17488	Q17488 caenorhabdi
23	103	17.4	1841	2	Q8MQG0	Q8mqg0 caenorhabdi
24	103	17.4	1867	2	Q17486	Q17486 caenorhabdi
25	103	17.4	2039	2	Q17489	Q17489 caenorhabdi
26	103	17.4	6994	2	Q17343	Q17343 caenorhabdi
27	103	17.4	6994	2	Q17490	Q17490 caenorhabdi
28	96.5	16.3	3924	1	ANK2_HUMAN	Q01484 homo sapien
29	93	15.7	324	1	TNR6_RAT	Q63199 rattus norv
30	91.5	15.4	965	2	Q7Z344	Q7z344 homo sapien
31	91.5	15.4	1863	2	Q7Z3L5	Q7z315 homo sapien
32	91	15.3	343	1	THO1_RAT	P59924 rattus norv
33	90.5	15.3	655	2	Q7SYB2	Q7syb2 brachydanio
34	90	15.2	186	2	Q7QJ06	Q7qj06 anopheles g
35	89.5	15.1	1038	2	Q80ZZ7	Q80zz7 mus musculu
36	89.5	15.1	1050	2	Q6PCN2	Q6pcn2 mus musculu
37	89.5	15.1	1050	2	Q8CCV0	Q8ccv0 mus musculu
38	89	15.0	293	2	Q9I9N5	Q9i9n5 brachydanio
39	87	14.7	332	1	TNR6_PIG	O77736 sus scrofa
40	87	14.7	1096	2	Q7UQT3	Q7uqt3 rhodopirell
41	86	14.5	143	2	O70510	O70510 rattus norv
42	86	14.5	811	2	Q9H0P5	Q9h0p5 homo sapien
43	86	14.5	838	2	Q9QXH1	Q9qxh1 mus musculu
44	86	14.5	960	2	Q8VDA0	Q8vda0 rattus norv
45	86	14.5	1093	2	Q8CBN3	Q8cbn3 mus musculu

ALIGNMENTS

RESULT 1
Q6LCB0
ID Q6LCB0 PRELIMINARY; PRT; 149 AA.
AC Q6LCB0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE FADD protein (Fragment).
GN Name=FADD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97113335; PubMed=8955195;
RA Kim P.K., Dutra A.S., Chandrasekharappa S.C., Puck J.M.;
RT "Genomic structure and mapping of human FADD, an intracellular
RT mediator of lymphocyte apoptosis.";
RL J. Immunol. 157:5461-5466(1996).
DR EMBL; U74301; AAB58483.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0042981; P:regulation of apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001875; DED.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF01335; DED; 1.
DR SMART; SM00005; DEATH; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50168; DED; 1.
FT NON_TER 1 1
SQ SEQUENCE 149 AA; 16696 MW; 3D8F7AB866127A41 CRC64;

Query Match 100.0%; Score 593; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 7.9e-47;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 82

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMS 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMS 138
```

RESULT 2
FADD_HUMAN
ID FADD_HUMAN STANDARD; PRT; 208 AA.
AC Q13158; Q14866;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   FADD protein (FAS-associating death domain-containing protein)
DE   (Mediator of receptor induced toxicity).
GN   Name=FADD; Synonyms=MORT1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=95277837; PubMed=7538907; DOI=10.1016/0092-8674(95)90071-3;
RA   Chinnaiyan A.M., O'Rourke K., Tewari M., Dixit V.M.;
RT   "FADD, a novel death domain-containing protein, interacts with the
RT   death domain of Fas and initiates apoptosis.";
RL   Cell 81:505-512(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95229578; PubMed=7536190; DOI=10.1074/jbc.270.14.7795;
RA   Boldin M.P., Varfolomeev E.E., Pancer Z., Mett I.L., Camonis J.H.,
RA   Wallach D.;
RT   "A novel protein that interacts with the death domain of Fas/APO1
RT   contains a sequence motif related to the death domain.";
RL   J. Biol. Chem. 270:7795-7798(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   INTERACTION WITH PEA15.
RX   MEDLINE=99369240; PubMed=10442631; DOI=10.1038/sj.onc.1202831;
RA   Condorelli G., Vigliotta G., Cafieri A., Trencia A., Andalo P.,
RA   Oriente F., Miele C., Caruso M., Formisano P., Beguinot F.;
RT   "PED/PEA-15: an anti-apoptotic molecule that regulates FAS/TNFR1-
RT   induced apoptosis.";
RL   Oncogene 18:4409-4415(1999).
RN   [5]
RP   INTERACTION WITH MBD4.
RX   PubMed=12702765; DOI=10.1073/pnas.0431215100;
RA   Screaton R.A., Kiessling S., Sansom O.J., Millar C.B., Maddison K.,
RA   Bird A., Clarke A.R., Frisch S.M.;
RT   "Fas-associated death domain protein interacts with methyl-CpG binding
RT   domain protein 4: a potential link between genome surveillance and
RT   apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:5211-5216(2003).
RN   [6]
RP   STRUCTURE BY NMR OF 1-83.
RX   MEDLINE=98241233; PubMed=9582077; DOI=10.1038/31972;
RA   Eberstadt M., Huang B., Chen Z., Meadows R.P., Ng S.C., Zheng L.,
RA   Lenardo M.J., Fesik S.W.;
RT   "NMR structure and mutagenesis of the FADD (Mort1) death-effector
RT   domain.";
RL   Nature 392:941-945(1998).
CC   -!- FUNCTION: Apoptotic adaptor molecule that recruits caspase-8 or
CC       caspase-10 to the activated Fas (CD95) or TNFR-1 receptors. The
CC       resulting aggregate called the death-inducing signaling complex
CC       (DISC) performs caspase-8 proteolytic activation. Active caspase-8
CC       initiates the subsequent cascade of caspases (aspartate-specific
CC       cysteine proteases) mediating apoptosis.
CC   -!- SUBUNIT: Interacts with CFLAR, PEA15 and MBD4.
CC   -!- TISSUE SPECIFICITY: Expressed in a wide variety of tissues, except
CC       for peripheral blood mononuclear leukocytes.
CC   -!- DOMAIN: Contains a death domain involved in the binding of the
CC       corresponding domain within Fas receptor.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- SIMILARITY: Contains 1 death effector (DED) domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U24231; AAA86517.1; -.
DR   EMBL; X84709; CAA59197.1; -.
DR   EMBL; BC000334; AAH00334.1; -.
DR   PIR; A56912; A56912.
DR   PDB; 1A1W; NMR; @=1-91.
DR   PDB; 1A1Z; NMR; @=1-91.
DR   PDB; 1E3Y; NMR; A=89-192.
DR   PDB; 1E41; NMR; A=89-192.
DR   Genew; HGNC:3573; FADD.
DR   H-InvDB; HIX0009893; -.
DR   MIM; 602457; -.
DR   GO; GO:0005123; F:death receptor binding; TAS.
DR   GO; GO:0004871; F:signal transducer activity; IEP.
DR   GO; GO:0008625; P:induction of apoptosis via death domain rec. . .; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
KW   3D-structure; Apoptosis.
FT   DOMAIN        3     81       DED.
FT   DOMAIN       97    181       Death.
FT   MUTAGEN     121    121       V->N: No interaction with Fas receptor.
FT   CONFLICT     32     32       G -> V (in Ref. 2).
FT   HELIX         3     28
FT   TURN         29     31
FT   HELIX        33     38
FT   HELIX        42     52
FT   TURN         53     53
FT   TURN         57     58
FT   HELIX        61     70
FT   TURN         71     71
FT   HELIX        73     81
FT   TURN         96     96
FT   HELIX        97    106
FT   TURN        107    107
FT   HELIX       112    120
FT   HELIX       123    132
FT   TURN        134    135
FT   HELIX       137    152
FT   HELIX       153    155
FT   HELIX       158    167
FT   TURN        168    169
FT   HELIX       171    185
FT   TURN        186    189
SQ   SEQUENCE   208 AA;  23279 MW;  0E65E2F852E83507 CRC64;

 Query Match             100.0%;  Score 593;  DB 1;  Length 208;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.1e-46;
  Matches  116;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 141

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMS 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMS 197


RESULT 3
Q645M6
ID   Q645M6      PRELIMINARY;      PRT;   209 AA.
AC   Q645M6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Fas-associated via death domain.
GN   Name=FADD;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Connor E.E., Szperka M.E., Bannerman D.D.;
RT   "Cloning and sequencing of the bovine Fas-associated death domain
RT   protein (FADD) cDNA.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Szperka M.E., Connor E.E., Paape M.J., Williams J.L., Bannerman D.D.;
RT   "Sequencing, chromosomal mapping, and functional characterization of
RT   bovine Fas-associated death domain (FADD) gene.";
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY725483; AAU20801.1; -.
SQ   SEQUENCE   209 AA;  23002 MW;  2EB6BA41F6DB0F9D CRC64;

  Query Match             65.6%;  Score 389;  DB 2;  Length 209;
  Best Local Similarity   65.5%;  Pred. No. 7.1e-28;
  Matches   76;  Conservative   18;  Mismatches   20;  Indels    2;  Gaps    1;

Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              || ||| |||| : || ||  :|||||||||||||| | ||| ||::||::||||| |:|
Db         82 FERGAAGGAAPEDRDLRAAMEIICDNVGKDWRRLARHLGVSDVKIEAIEEKYPRNLAEQV 141

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPMS 116
              || ||:|||: :||| |: |||||| ||:|:||||::| |:|| ||  ||: :| |
Db        142 RELLRVWKNSTRENAAVSCLVGALRGCQLNVVADLIEEDQRARALQ--SGSANPGS 195


RESULT 4
FADD_MOUSE
ID   FADD_MOUSE     STANDARD;      PRT;   205 AA.
AC   Q61160; Q61082;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   FADD protein (FAS-associating death domain-containing protein)
DE   (Mediator of receptor induced toxicity).
GN   Name=Fadd; Synonyms=Mort1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96220459; PubMed=8649383;
RA   Zhang J., Winoto A.;
RT   "A mouse Fas-associated protein with homology to the human Mort1/FADD
RT   protein is essential for Fas-induced apoptosis.";
RL   Mol. Cell. Biol. 16:2756-2763(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96152659; PubMed=8565075; DOI=10.1016/S0092-8674(00)80984-8;
RA   Hsu H., Shu H.-B., Pan M.G., Goeddel D.V.;
RT   "TRADD-TRAF2 and TRADD-FADD interactions define two distinct TNF
RT   receptor 1 signal transduction pathways.";
RL   Cell 84:299-308(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Heart;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Czech II; TISSUE=Mammary gland, and Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   STRUCTURE BY NMR OF 89-183.
RX   PubMed=10347191; DOI=10.1074/jbc.274.23.16337;
RA   Jeong E.-J., Bang S., Lee T.H., Park Y.-I., Sim W.-S., Kim K.-S.;
RT   "The solution structure of FADD death domain. Structural basis of
RT   death domain interactions of Fas and FADD.";
RL   J. Biol. Chem. 274:16337-16342(1999).
```

```
CC   -!- FUNCTION: Apoptotic adaptor molecule that recruits caspase-8 or
CC       caspase-10 to the activated Fas (CD95) or TNFR-1 receptors. The
CC       resulting aggregate called the death-inducing signaling complex
CC       (DISC) performs caspase-8 proteolytic activation. Active caspase-8
CC       initiates the subsequent cascade of caspases (aspartate-specific
CC       cysteine proteases) mediating apoptosis (By similarity).
CC   -!- SUBUNIT: Interacts with CFLAR, PEA15 and MBD4 (By similarity).
CC   -!- DOMAIN: Contains a death domain involved in the binding of the
CC       corresponding domain within Fas receptor.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   -!- SIMILARITY: Contains 1 death effector (DED) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U50406; AAB07789.1; -.
DR   EMBL; U43184; AAA97876.1; -.
DR   EMBL; AK084808; BAC39283.1; -.
DR   EMBL; BC004584; AAH04584.1; -.
DR   EMBL; BC021400; AAH21400.1; -.
DR   PDB; 1FAD; NMR; A=85-183.
DR   MGD; MGI:109324; Fadd.
DR   GO; GO:0008632; P:apoptotic program; IMP.
DR   GO; GO:0042981; P:regulation of apoptosis; IMP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
KW   3D-structure; Apoptosis.
FT   DOMAIN        3     81       DED.
FT   DOMAIN       97    181       Death.
FT   CONFLICT    168    168       C -> F (in Ref. 2).
FT   TURN         92     93
FT   HELIX        94    118
FT   TURN        119    120
FT   HELIX       123    132
FT   HELIX       137    152
FT   HELIX       153    156
FT   HELIX       158    168
FT   TURN        169    169
FT   HELIX       171    181
SQ   SEQUENCE   205 AA;  22960 MW;  4BC8D86B33A58783 CRC64;

  Query Match             64.5%;  Score 382.5;  DB 1;  Length 205;
  Best Local Similarity   61.7%;  Pred. No. 2.8e-27;
  Matches   71;  Conservative   25;  Mismatches   16;  Indels    3;  Gaps    1;

Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              |||| |  | ||| ||  ||:::|||||:||:||||:||||: |:| ||::|||:|:|||
Db         82 FEAGTATAAPPGEADLQVAFDIVCDNVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERV 141

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPM 115
              ||||::||| ||:||:|| || |||:|::|||||||:| |::    ::|  |||:
Db        142 RESLKVWKNAEKKNASVAGLVKALRTCRLNLVADLVEEAQES---VSKSENMSPV 193


RESULT 5
Q8CD57
ID   Q8CD57      PRELIMINARY;      PRT;   205 AA.
AC   Q8CD57;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE   enriched library, clone:6030422N02 product:Fas-associated via death
DE   domain, full insert sequence.
GN   Name=Fadd;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK031396; BAC27384.1; -.
DR   HSSP; Q61160; 1FAD.
DR   MGD; MGI:109324; Fadd.
DR   GO; GO:0008632; P:apoptotic program; IMP.
DR   GO; GO:0042981; P:regulation of apoptosis; IMP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
```

```
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00031; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
SQ   SEQUENCE   205 AA;  22891 MW;  4A8DD86B32E08776 CRC64;

  Query Match             64.5%;  Score 382.5;  DB 2;  Length 205;
  Best Local Similarity   61.7%;  Pred. No. 2.8e-27;
  Matches   71;  Conservative   25;  Mismatches   16;  Indels    3;  Gaps    1;

Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              |||| |  | ||| ||  ||:::|||||:||:||||:||||: |:| ||::|||:|:|||
Db         82 FEAGTATAAPPGEADLQVAFDIVCDNVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERV 141

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGAMSPM 115
              ||||::||| ||:||:|| || |||:|::|||||||:| |::    ::|  |||:
Db        142 RESLKVWKNAEKKNASVAGLVKALRTCRLNLVADLVEEAQES---VSKSENMSPV 193


RESULT 6
Q8R2E7
ID   Q8R2E7      PRELIMINARY;      PRT;   208 AA.
AC   Q8R2E7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fas death domain associated protein (FADD/MORT1 protein with death
DE   effector domain).
GN   Name=fadd;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Ischemic brain;
RA   Spadoni C.G.;
RT   "Identification of neuronal caspases and involvement of death domain
RT   proteins in neuronal apoptosis.";
RL   Thesis (2001), University of London, London, United Kingdom.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Ischemic brain;
RA   Neame S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=22254898; PubMed=12167637; DOI=10.1074/jbc.M203484200;
RA   Kim P.K.M., Wang Y., Gambotto A., Kim Y.M., Weller R.,
RA   Zuckerbraun B.S., Hua Y., Watkins S.C., Billiar T.R.;
RT   "Hepatocyte Fas-associating death domain protein/mediator of receptor-
RT   induced toxicity (FADD/MORT1) levels increase in response to pro-
RT   apoptotic stimuli.";
RL   J. Biol. Chem. 277:38855-38862(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RA   Kim P.K., Billiar T.R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ441127; CAD29628.1; -.
DR   EMBL; AF406779; AAN01113.1; -.
DR   HSSP; Q61160; 1FAD.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00031; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
SQ   SEQUENCE   208 AA;  23124 MW;  ABA3305406137CDB CRC64;

  Query Match             64.2%;  Score 381;  DB 2;  Length 208;
  Best Local Similarity   64.2%;  Pred. No. 3.9e-27;
  Matches   70;  Conservative   21;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 FEAGAAAGAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERV 60
              |||||    | ||| ||  ||:::|||||:||:||||:||||: ||| ||:||||:|::||
Db         82 FEAGATTAATPGEADLRVAFDIVCDNVGRDWKRLARELKVSEAKIDGIEERYPRSLSDRV 141

Qy         61 RESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRS 109
              ||:||:||| |||||:|| || |||:|::||||||||:|    |:   ::|
Db        142 RETLRVWKNVEKENASVAGLVKALRACRLNLVADLVEEALMAQGSVSKS 190


RESULT 7
Q6Q782
ID   Q6Q782      PRELIMINARY;      PRT;   189 AA.
AC   Q6Q782;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fas-associated death domain.
OS   Ictalurus punctatus (Channel catfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC   Ictaluridae; Ictalurus.
OX   NCBI_TaxID=7998;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20069572; PubMed=10602874; DOI=10.1007/s002510050588;
RA   Hawke N.A., Yoder J.A., Litman G.W.;
RT   "Expanding our understanding of immunoglobulin, T-cell antigen
RT   receptor, and novel immune-type receptor genes: a subset of the
RT   immunoglobulin gene superfamily.";
RL   Immunogenetics 50:124-133(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Long S., Wilson M.R., Bengten E., Hawke N.A., Clem L.W., Miller N.W.,
RA   Chinchar V.G.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY555194; AAS84609.1; -.
DR   HSSP; Q13158; 1A1W.
DR   GO; GO:0005515; F:protein binding; IEA.
DR   GO; GO:0042981; P:regulation of apoptosis; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001875; DED.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF01335; DED; 1.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00031; DED; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50168; DED; 1.
SQ   SEQUENCE   189 AA;  22240 MW;  63E85FAD3D2E14A9 CRC64;

  Query Match             31.9%;  Score 189;  DB 2;  Length 189;
  Best Local Similarity   39.6%;  Pred. No. 1.7e-09;
  Matches   38;  Conservative   22;  Mismatches   32;  Indels    4;  Gaps    2;

Qy         11 PGE---EDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW 67
              | |   | :  |  || : :|: | :  |:||:::||:: |::::|||| |:|||  : |
Db         91 PNETELEKINCAIEVISEQLGRKWIKYGRKLKIAETKLEGIQEKHPRNLEEQVREWPKEW 150

Qy         68 KNTEKENATVAHLVGALRSCQMNLVADLVQ-EVQQA 102
                 | | |: ||| | :|  ||:||  :|:|
Db        151 MKMHKAEAKVDELIRALRDCTLNYTADVVQMNLQKA 186
```

```
RESULT 8
RIK1_MOUSE
ID   RIK1_MOUSE     STANDARD;      PRT;   656 AA.
AC   Q60855; Q8CD90;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Receptor-interacting serine/threonine-protein kinase 2 (EC 2.7.1.37)
DE   (Serine/threonine-protein kinase RIP) (Cell death protein RIP)
DE   (Receptor interacting protein).
GN   Name=Ripk1; Synonyms=Rinp, RIP;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX   MEDLINE=95277838; PubMed=7538908; DOI=10.1016/0092-8674(95)90072-1;
RA   Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT   "RIP: a novel protein containing a death domain that interacts with
RT   Fas/APO-1 (CD95) in yeast and causes cell death.";
RL   Cell 81:513-523(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain, and Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.
CC       Required for TNFRSF1A mediated activation of NF-kappa-B.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is
CC       recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds
CC       RIPK3, UBCE7IP1, EGFR, IKBKG, TRAF1, TRAF2 and TRAF3. Interacts
CC       with BNLF1 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Found at low levels in all tissues.
CC   -!- INDUCTION: In concanavalin A-treated splenocytes.
CC   -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced
CC       apoptosis. Cleavage abolishes NF-kappa-B activation and enhances
CC       pro-apototic signaling through the TRADD-FADD interaction (By
CC       similarity).
CC   -!- PTM: Autophosphorylated on serine and threonine residues (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U25995; AAB60487.1; -.
DR   EMBL; AK030959; BAC27194.1; -.
DR   EMBL; BC050905; AAH50905.1; ALT_INIT.
DR   EMBL; BC054542; AAH54542.1; -.
DR   EMBL; BC058162; AAH58162.1; -.
DR   PIR; I49299; I49299.
DR   HSSP; Q13158; 1E41.
DR   MGD; MGI:108212; Ripk1.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Apoptosis; ATP-binding; Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       17    290       Protein kinase.
FT   NP_BIND      23     31       ATP (By similarity).
FT   BINDING      46     46       ATP (By similarity).
FT   ACT_SITE    138    138       Proton acceptor (By similarity).
FT   DOMAIN      568    654       Death.
FT   VARIANT     473    473       T -> I.
FT   CONFLICT     66     66       M -> K (in Ref. 2).
SQ   SEQUENCE   656 AA;  74854 MW;  ABB350B523879933 CRC64;

  Query Match             19.5%;  Score 115.5;  DB 1;  Length 656;
  Best Local Similarity   34.9%;  Pred. No. 0.04;
  Matches   29;  Conservative   22;  Mismatches   29;  Indels    3;  Gaps    3;

Qy         21 NVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRN-LTERVRESLRIWKNTE-KENATVA 78
              | | :|:|: |:  ||:|  ::::|| |:  | |: | |:| : |: |   |  : |||
```

```
Db        573 NPIRENLGRQWKNCARKLGFTESQIDEIDHDYERDGLKEKVYQMLQKWLMREGTKGATVG 632

Qy         79 HLVGAL-RSCQMNLVADLVQEVQ 100
                 |  || : |:::|:  |::  |
Db        633 KLAQALHQCCRIDLLNHLIRASQ 655


RESULT 9
Q13768
ID   Q13768      PRELIMINARY;      PRT;  1719 AA.
AC   Q13768;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alt. ankyrin (Variant 2.2).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Hematopoietic;
RX   MEDLINE=90158830; PubMed=2137557;
RA   Lux S.E., John K.M., Bennett V.;
RT   "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT   structure with homology to tissue-differentiation and cell-cycle
RT   control proteins.";
RL   Nature 344:36-42(1990).
DR   EMBL; X16609; CAA34611.1; -.
DR   HSSP; P16157; 1N11.
DR   GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR   GO; GO:0005856; C:cytoskeleton; NAS.
DR   GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR   GO; GO:0019899; F:enzyme binding; ISS.
DR   GO; GO:0030507; F:spectrin binding; ISS.
DR   GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR   GO; GO:0006887; P:exocytosis; NAS.
DR   GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00023; Ank; 23.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 23.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00218; ZU5; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 20.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   ANK repeat.
SQ   SEQUENCE   1719 AA;  189010 MW;  F63465D16D975CBF CRC64;

  Query Match             19.3%;  Score 114.5;  DB 2;  Length 1719;
  Best Local Similarity   28.1%;  Pred. No. 0.14;
  Matches   32;  Conservative   26;  Mismatches   49;  Indels    7;  Gaps    2;

Qy          8 GAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW 67
              |:  | |        || :::|  |  |||:|: |   |: |    | :| |:    | :|
Db       1395 GSLSGTEQAEMKMAVISEHLGLSWAELARELQFSVEDINRIRVENPNSLLEQSVALLNLW 1454

Qy         68 KNTEKENATVAHLVGALRSCQMNLVADLVQ-EVQQARDLQ------NRSGAMSP 114
                | :|| : :|  ||:|     : ::::   :|:|:|:      :|  ::||
Db       1455 VIREGQNANMENLYTALQSIDRGEIVNMLEGSGRQSRNLKPDRRHTDRDYSLSP 1508


RESULT 10
Q99407
ID   Q99407      PRELIMINARY;      PRT;  1856 AA.
AC   Q99407;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ankyrin.
GN   Name=ANK1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97382244; PubMed=9235914; DOI=10.1074/jbc.272.31.19220;
RA   Gallagher P.G., Tse W.T., Scarpa A.L., Lux S.E., Forget B.G.;
RT   "Structure and organization of the human ankyrin-1 gene. Basis for
RT   complexity of pre-mRNA processing.";
RL   J. Biol. Chem. 272:19220-19228(1997).
DR   EMBL; U50092; AAB47805.1; JOINED.
DR   EMBL; U50093; AAB47805.1; JOINED.
DR   EMBL; U50094; AAB47805.1; JOINED.
DR   EMBL; U50095; AAB47805.1; JOINED.
DR   EMBL; U50096; AAB47805.1; JOINED.
DR   EMBL; U50097; AAB47805.1; JOINED.
DR   EMBL; U50098; AAB47805.1; JOINED.
DR   EMBL; U50099; AAB47805.1; JOINED.
DR   EMBL; U50100; AAB47805.1; JOINED.
DR   EMBL; U50133; AAB47805.1; -.
DR   EMBL; U50101; AAB47805.1; JOINED.
DR   EMBL; U50102; AAB47805.1; JOINED.
DR   EMBL; U50103; AAB47805.1; JOINED.
DR   EMBL; U50104; AAB47805.1; JOINED.
DR   EMBL; U50105; AAB47805.1; JOINED.
DR   EMBL; U50106; AAB47805.1; JOINED.
DR   EMBL; U50107; AAB47805.1; JOINED.
DR   EMBL; U50108; AAB47805.1; JOINED.
DR   EMBL; U50109; AAB47805.1; JOINED.
DR   EMBL; U50110; AAB47805.1; JOINED.
DR   EMBL; U50111; AAB47805.1; JOINED.
DR   EMBL; U50112; AAB47805.1; JOINED.
DR   EMBL; U50113; AAB47805.1; JOINED.
DR   EMBL; U50114; AAB47805.1; JOINED.
DR   EMBL; U50115; AAB47805.1; JOINED.
DR   EMBL; U50116; AAB47805.1; JOINED.
DR   EMBL; U50117; AAB47805.1; JOINED.
DR   EMBL; U50118; AAB47805.1; JOINED.
DR   EMBL; U50119; AAB47805.1; JOINED.
DR   EMBL; U50120; AAB47805.1; JOINED.
DR   EMBL; U50121; AAB47805.1; JOINED.
DR   EMBL; U50122; AAB47805.1; JOINED.
DR   EMBL; U50123; AAB47805.1; JOINED.
DR   EMBL; U50124; AAB47805.1; JOINED.
DR   EMBL; U50125; AAB47805.1; JOINED.
DR   EMBL; U50126; AAB47805.1; JOINED.
DR   EMBL; U50127; AAB47805.1; JOINED.
DR   EMBL; U50128; AAB47805.1; JOINED.
DR   EMBL; U50129; AAB47805.1; JOINED.
DR   EMBL; U50130; AAB47805.1; JOINED.
DR   EMBL; U50131; AAB47805.1; JOINED.
DR   EMBL; U50132; AAB47805.1; JOINED.
DR   HSSP; P16157; 1N11.
DR   GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR   GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR   GO; GO:0019899; F:enzyme binding; ISS.
DR   GO; GO:0030507; F:spectrin binding; ISS.
DR   GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR   GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00023; Ank; 22.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 22.
```

```
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00218; ZU5; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 20.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   ANK repeat.
SQ   SEQUENCE   1856 AA;  203465 MW;  4A4E3A794DD6401F CRC64;

  Query Match             19.3%;  Score 114.5;  DB 2;  Length 1856;
  Best Local Similarity   28.1%;  Pred. No. 0.16;
  Matches   32;  Conservative   26;  Mismatches   49;  Indels    7;  Gaps    2;

Qy          8 GAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW 67
              |:  | |        || :::|  |  |||:|: |   |: |    | :| |:   | :|
Db       1370 GSLSGTEQAEMKMAVISEHLGLSWAELARELQFSVEDINRIRVENPNSLLEQSVALLNLW 1429

Qy         68 KNTEKENATVAHLVGALRSCQMNLVADLVQ-EVQQARDLQ------NRSGAMSP 114
                | :|| : :|  ||:|     : ::::   :|:|:|:      :|  ::||
Db       1430 VIREGQNANMENLYTALQSIDRGEIVNMLEGSGRQSRNLKPDRRHTDRDYSLSP 1483


RESULT 11
ANK1_HUMAN
ID   ANK1_HUMAN     STANDARD;      PRT;  1880 AA.
AC   P16157;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R).
GN   Name=ANK1; Synonyms=ANK;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.
RC   TISSUE=Hematopoietic;
RX   MEDLINE=90158830; PubMed=2137557;
RA   Lux S.E., John K.M., Bennett V.;
RT   "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
RT   structure with homology to tissue-differentiation and cell-cycle
RT   control proteins.";
RL   Nature 344:36-42(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90175370; PubMed=1689849;
RA   Lambert S., Yu H., Prchal J.T., Lawler J., Ruff P., Speicher D.,
RA   Cheung M.C., Kan Y.W., Palek J.;
RT   "cDNA sequence for human erythrocyte ankyrin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
RN   [3]
RP   VARIANT HS ILE-462.
RX   MEDLINE=96225450; PubMed=8640229;
RA   Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
RA   Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
RA   Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
RT   "Ankyrin-1 mutations are a major cause of dominant and recessive
RT   hereditary spherocytosis.";
RL   Nat. Genet. 13:214-218(1996).
CC   -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC       elements; bind to the erythrocyte membrane protein band 4.2, to
CC       Na-K ATPase, to the lymphocyte membrane protein GP85, and to the
CC       cytoskeletal proteins fodrin, tubulin, vimentin and desmin.
CC       Erythrocyte ankyrins also link spectrin (beta chain) to the
CC       cytoplasmic domain of the erythrocytes anion exchange protein;
CC       they retain most or all of these binding functions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocytic plasma
CC       membrane.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=2.1;
CC         IsoId=P16157-1; Sequence=Displayed;
CC       Name=2; Synonyms=2.2;
CC         IsoId=P16157-2; Sequence=VSP_000264, VSP_000265;
CC       Name=3;
CC         IsoId=P16157-3; Sequence=VSP_000266;
CC   -!- PTM: Regulated by phosphorylation.
CC   -!- PTM: Palmitoylated.
CC   -!- DISEASE: Defects in ANK1 are a cause of hereditary spherocytosis
CC       (HS) [MIM:182900]. Inheritance can be autosomal dominant or
CC       recessive.
CC   -!- SIMILARITY: Contains 23 ANK repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X16609; CAA34610.1; -.
DR   EMBL; M28880; AAA51732.1; -.
DR   PIR; A35049; A35049.
DR   PIR; S08275; SJHUK.
DR   PDB; 1N11; X-ray; A=390-826.
DR   Genew; HGNC:492; ANK1.
DR   MIM; 182900; -.
DR   GO; GO:0016323; C:basolateral plasma membrane; NAS.
DR   GO; GO:0008093; F:cytoskeletal adaptor activity; TAS.
DR   GO; GO:0019899; F:enzyme binding; TAS.
DR   GO; GO:0030507; F:spectrin binding; NAS.
DR   GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
DR   GO; GO:0045199; P:maintenance of epithelial cell polarity; TAS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00023; Ank; 23.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 20.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   3D-structure; Alternative splicing; ANK repeat; Cytoskeleton;
KW   Direct protein sequencing; Disease mutation; Elliptocytosis;
KW   Lipoprotein; Phosphorylation; Polymorphism; Repeat.
FT   INIT_MET      0      0
FT   DOMAIN        1    826       89 kDa domain; anion exchange protein
FT                                binding domain.
FT   DOMAIN      827   1381       62 kDa domain; spectrin binding domain.
FT   DOMAIN     1382   1880       55 kDa regulatory domain; regulates the
FT                                binding of ankyrin to spectrin and the
FT                                band 3 protein.
FT   REPEAT       43     72       ANK 1.
FT   REPEAT       76    105       ANK 2.
FT   REPEAT      109    138       ANK 3.
FT   REPEAT      142    171       ANK 4.
FT   REPEAT      173    200       ANK 5.
FT   REPEAT      204    233       ANK 6.
FT   REPEAT      237    266       ANK 7.
FT   REPEAT      270    299       ANK 8.
FT   REPEAT      303    332       ANK 9.
FT   REPEAT      336    365       ANK 10.
FT   REPEAT      369    398       ANK 11.
FT   REPEAT      402    431       ANK 12.
FT   REPEAT      435    464       ANK 13.
FT   REPEAT      468    497       ANK 14.
FT   REPEAT      501    530       ANK 15.
FT   REPEAT      534    563       ANK 16.
FT   REPEAT      567    596       ANK 17.
FT   REPEAT      600    629       ANK 18.
FT   REPEAT      633    662       ANK 19.
```

```
FT   REPEAT      666    695       ANK 20.
FT   REPEAT      699    728       ANK 21.
FT   REPEAT      732    761       ANK 22.
FT   REPEAT      765    794       ANK 23.
FT   DOMAIN     1402   1486       Death.
FT   VARSPLIC   1512   1873       Missing (in isoform 2).
FT                                /FTId=VSP_000264.
FT   VARSPLIC   1874   1874       H -> D (in isoform 2).
FT                                /FTId=VSP_000265.
FT   VARSPLIC   1849   1880       TVEGPLEDPSELEVDIDYFMKHSKDHTSTPNP -> ELRGS
FT                                GLQPDLIEGRKGAQIVKRASLKRGKQ (in isoform
FT                                3).
FT                                /FTId=VSP_000266.
FT   VARIANT      20     20       R -> T.
FT                                /FTId=VAR_000595.
FT   VARIANT     462    462       V -> I (in HS).
FT                                /FTId=VAR_000596.
FT   VARIANT     618    618       R -> H (in Brueggen).
FT                                /FTId=VAR_000597.
FT   VARIANT     749    749       V -> A.
FT                                /FTId=VAR_000598.
FT   VARIANT     844    844       D -> E.
FT                                /FTId=VAR_000599.
FT   VARIANT    1285   1285       E -> D.
FT                                /FTId=VAR_000601.
FT   VARIANT    1391   1391       S -> T.
FT                                /FTId=VAR_000600.
FT   VARIANT    1591   1591       D -> N (in Duesseldorf).
FT                                /FTId=VAR_000602.
FT   VARIANT    1698   1698       R -> D.
FT                                /FTId=VAR_000603.
FT   CONFLICT    229    229       A -> S (in Ref. 2).
FT   CONFLICT   1545   1545       V -> I (in Ref. 2).
SQ   SEQUENCE   1880 AA;  206145 MW;  1C5F5E7EFD1CD428 CRC64;

  Query Match             19.3%;  Score 114.5;  DB 1;  Length 1880;
  Best Local Similarity   28.1%;  Pred. No. 0.16;
  Matches   32;  Conservative   26;  Mismatches   49;  Indels    7;  Gaps    2;

Qy          8 GAAPGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIW 67
              |:  | |        || :::|  |  |||:|: |   |: |    | :| |:    | :|
Db       1394 GSLSGTEQAEMKMAVISEHLGLSWAELARELQFSVEDINRIRVENPNSLLEQSVALLNLW 1453

Qy         68 KNTEKENATVAHLVGALRSCQMNLVADLVQ-EVQQARDLQ------NRSGAMSP 114
                | :|| : :|  ||:|     : ::::   :|:|:|:      :|  ::||
Db       1454 VIREGQNANMENLYTALQSIDRGEIVNMLEGSGRQSRNLKPDRRHTDRDYSLSP 1507


RESULT 12
Q9V3B4
ID   Q9V3B4      PRELIMINARY;      PRT;   239 AA.
AC   Q9V3B4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CG12297-PA (Death domain-containing adaptor protein) (Death-domain
DE   containing protein BG4).
GN   Name=BG4; ORFNames=CG12297;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA   Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RG   FlyBase;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
```

```
RN   [7]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20469420; PubMed=10934188; DOI=10.1074/jbc.C000341200;
RA   Hu S., Yang X.;
RT   "dFADD, a novel death domain-containing adapter protein for the
RT   Drosophila caspase DREDD.";
RL   J. Biol. Chem. 275:30761-30764(2000).
RN   [8]
RP   SEQUENCE FROM N.A.
RA   Zhou L., Steller H.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003737; AAF55950.1; -.
DR   EMBL; AF295103; AAG22535.1; -.
DR   EMBL; AF222005; AAF44325.1; -.
DR   HSSP; Q61160; 1FAD.
DR   IntAct; Q9V3B4; -.
DR   FlyBase; FBgn0038928; BG4.
DR   GO; GO:0005515; F:protein binding; TAS.
DR   GO; GO:0050829; P:defense response to Gram-negative bacteria; TAS.
DR   GO; GO:0006955; P:immune response; IMP.
DR   GO; GO:0007291; P:sperm individualization; IMP.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   Pfam; PF00531; Death; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
SQ   SEQUENCE   239 AA;  27421 MW;  F43CFAA546C3FCD9 CRC64;

  Query Match             19.2%;  Score 114;  DB 2;  Length 239;
  Best Local Similarity   26.8%;  Pred. No. 0.018;
  Matches   34;  Conservative   22;  Mismatches   37;  Indels   34;  Gaps    4;

Qy          3 AGAAAGAAPGEEDLCAA----------------------FNVICDNVGKDWRRLARQLK 39
              | |:  | |   :| ||                        |  | : :|: |||| |
Db        115 APASQNAQPSVSELAAAVPPTAIQNYATPAAFTDHKRTMVFKKISEELGRYWRRLGRSAG 174

Qy         40 VSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENA-----TVAHLVGALRSCQMNLVAD 94
              : : ::|:||:||| :|  ::   ||: :  |:::      :  |  ||  |  |   |
Db        175 IGEGQMDTIEERYPHDLKSQI---LRLLQLIEEDDCHDPKHFLLRLCRALGDCGRN---D 228

Qy         95 LVQEVQQ 101
              | : |:|
Db        229 LRKRVEQ 235


RESULT 13
Q61302
ID   Q61302      PRELIMINARY;      PRT;  1848 AA.
AC   Q61302;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Erythroid ankyrin.
GN   Name=Ank1; Synonyms=Ank-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Neural;
RX   MEDLINE=93252825; PubMed=8486643;
RA   Birkenmeier C.S., White R.A., Peters L.L., Hall E.J., Lux S.E.,
RA   Barker J.E.;
RT   "Complex patterns of sequence variation and multiple 5' and 3' ends
RT   are found among transcripts of the erythroid ankyrin gene.";
RL   J. Biol. Chem. 268:9533-9540(1993).
DR   EMBL; X69063; CAA48801.1; -.
DR   PIR; S37771; S37771.
DR   HSSP; P16157; 1N11.
DR   MGD; MGI:88024; Ank1.
DR   GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR   GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR   GO; GO:0019899; F:enzyme binding; ISS.
DR   GO; GO:0030507; F:spectrin binding; ISS.
DR   GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR   GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00023; Ank; 23.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 23.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00218; ZU5; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 20.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   ANK repeat.
SQ   SEQUENCE   1848 AA;  202576 MW;  5744BECBF9EBA056 CRC64;

  Query Match             19.0%;  Score 112.5;  DB 2;  Length 1848;
  Best Local Similarity   29.0%;  Pred. No. 0.24;
  Matches   29;  Conservative   27;  Mismatches   37;  Indels    7;  Gaps    2;

Qy         22 VICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLV 81
              || :::|  |  |||:|: |   |: |    | :| ::    | :| : | ||| : :|
Db       1421 VIREHLGLSWAELARELQFSVEDINRIRVENPNSLLDQSTALLTLWVDREGENAKMENLY 1480

Qy         82 GALRSCQMNLVADLVQ-EVQQARDLQ------NRSGAMSP 114
              |||:   : : ::::   :|:|:|:      :|  ::||
Db       1481 TALRNIDRSEIVNMLEVSGRQSRNLKPERRHGDREYSLSP 1520


RESULT 14
ANK1_MOUSE
ID   ANK1_MOUSE     STANDARD;      PRT;  1862 AA.
AC   Q02357;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Ankyrin 1 (Erythrocyte ankyrin).
GN   Name=Ank1; Synonyms=Ank-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Erythrocyte;
RX   MEDLINE=92345717; PubMed=1386265;
RA   White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT   "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
RT   regulatory domain.";
RL   Mamm. Genome 3:281-285(1992).
CC   -!- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC       elements; bind to the erythrocyte membrane protein band 4.2, to
CC       Na-K ATPase, to the lymphocyte membrane protein GP85, and to the
CC       cytoskeletal proteins fodrin, tubulin, vimentin and desmin.
CC       Erythrocyte ankyrins also link spectrin (beta chain) to the
CC       cytoplasmic domain of the erythrocytes anion exchange protein;
CC       they retain most or all of these binding functions.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic surface of erythrocytic plasma
CC       membrane.
CC   -!- PTM: Regulated by phosphorylation (By similarity).
CC   -!- PTM: Acylated by palmitic acid group(s) (By similarity).
CC   -!- SIMILARITY: Contains 23 ANK repeats.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
```

```
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M84756; AAA37236.1; -.
DR   PIR; I49502; I49502.
DR   HSSP; P16157; 1N11.
DR   MGD; MGI:88024; Ank1.
DR   GO; GO:0016323; C:basolateral plasma membrane; ISS.
DR   GO; GO:0008093; F:cytoskeletal adaptor activity; ISS.
DR   GO; GO:0019899; F:enzyme binding; ISS.
DR   GO; GO:0030507; F:spectrin binding; ISS.
DR   GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
DR   GO; GO:0045199; P:maintenance of epithelial cell polarity; ISS.
DR   InterPro; IPR002110; ANK.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR000906; ZU5.
DR   Pfam; PF00023; Ank; 23.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00791; ZU5; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   SMART; SM00248; ANK; 23.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00218; ZU5; 1.
DR   PROSITE; PS50297; ANK_REP_REGION; 1.
DR   PROSITE; PS50088; ANK_REPEAT; 20.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
KW   ANK repeat; Cytoskeleton; Lipoprotein; Phosphorylation; Repeat.
FT   DOMAIN        1    827       89 kDa domain; anion exchange protein
FT                                binding domain.
FT   DOMAIN      828   1386       62 kDa domain; spectrin binding domain.
FT   DOMAIN     1387   1862       55 kDa regulatory domain; regulates the
FT                                binding of ankyrin to spectrin and the
FT                                band 3 protein.
FT   REPEAT       40     69       ANK 1.
FT   REPEAT       73    102       ANK 2.
FT   REPEAT      106    135       ANK 3.
FT   REPEAT      139    168       ANK 4.
FT   REPEAT      170    197       ANK 5.
FT   REPEAT      201    230       ANK 6.
FT   REPEAT      234    263       ANK 7.
FT   REPEAT      267    296       ANK 8.
FT   REPEAT      300    329       ANK 9.
FT   REPEAT      333    362       ANK 10.
FT   REPEAT      366    395       ANK 11.
FT   REPEAT      399    428       ANK 12.
FT   REPEAT      432    461       ANK 13.
FT   REPEAT      465    494       ANK 14.
FT   REPEAT      498    527       ANK 15.
FT   REPEAT      531    560       ANK 16.
FT   REPEAT      564    593       ANK 17.
FT   REPEAT      597    626       ANK 18.
FT   REPEAT      630    659       ANK 19.
FT   REPEAT      663    692       ANK 20.
FT   REPEAT      696    725       ANK 21.
FT   REPEAT      729    758       ANK 22.
FT   REPEAT      762    791       ANK 23.
FT   DOMAIN     1399   1483       Death.
SQ   SEQUENCE   1862 AA;  204242 MW;  AE6B85B5B29001E5 CRC64;

  Query Match             19.0%;  Score 112.5;  DB 1;  Length 1862;
  Best Local Similarity   29.0%;  Pred. No. 0.24;
  Matches   29;  Conservative   27;  Mismatches   37;  Indels    7;  Gaps    2;

Qy         22 VICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLV 81
              || :::|  |  |||:|: |   |: |    | :| ::    | :| : | ||| : :|
Db       1405 VIREHLGLSWAELARELQFSVEDINRIRVENPNSLLDQSTALLTLWVDREGENAKMENLY 1464

Qy         82 GALRSCQMNLVADLVQ-EVQQARDLQ------NRSGAMSP 114
                |||:   : : ::::   :|:|:|:      :|  ::||
Db       1465 TALRNIDRSEIVNMLEGSGRQSRNLKPERRHGDREYSLSP 1504
```

```
RESULT 15
RIK1_HUMAN
ID   RIK1_HUMAN     STANDARD;      PRT;   671 AA.
AC   Q13546; Q13180;
DT   01-NOV-1997 (Rel. 35, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Receptor-interacting serine/threonine-protein kinase 2 (EC 2.7.1.37)
DE   (Serine/threonine-protein kinase RIP) (Cell death protein RIP)
DE   (Receptor interacting protein).
GN   Name=RIPK1; Synonyms=RIP;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AUTOPHOSPHORYLATION, MUTAGENESIS OF LYS-45, AND
RP   INTERACTIONS WITH TRADD; TRAF1; TRAF2 AND TRAF3.
RC   TISSUE=Umbilical vein endothelial cells;
RX   MEDLINE=96200892; PubMed=8612133; DOI=10.1016/S1074-7613(00)80252-6;
RA   Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
RT   "TNF-dependent recruitment of the protein kinase RIP to the TNF
RT   receptor-1 signaling complex.";
RL   Immunity 4:387-396(1996).
RN   [2]
RP   REVISION TO 120.
RA   Huang J., Hsu H., Baichwal V.R., Goeddel D.V.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Sycamore N.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 300-671 FROM N.A.
RC   TISSUE=Leukemic T-cell;
RX   MEDLINE=95277838; PubMed=7538908; DOI=10.1016/0092-8674(95)90072-1;
RA   Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT   "RIP: a novel protein containing a death domain that interacts with
RT   Fas/APO-1 (CD95) in yeast and causes cell death.";
RL   Cell 81:513-523(1995).
RN   [5]
RP   CLEAVAGE BY CASPASE-8, AND MUTAGENESIS OF ASP-324.
RX   MEDLINE=99452794; PubMed=10521396; DOI=10.1101/gad.13.19.2514;
RA   Lin Y., Devin A., Rodriguez Y., Liu Z.-G.;
RT   "Cleavage of the death domain kinase RIP by caspase-8 prompts TNF-
RT   induced apoptosis.";
RL   Genes Dev. 13:2514-2526(1999).
RN   [6]
RP   INTERACTION WITH RIPK3.
RX   MEDLINE=99287880; PubMed=10358032; DOI=10.1074/jbc.274.24.16871;
RA   Sun X., Lee J., Navas T., Baldwin D.T., Stewart T.A., Dixit V.M.;
RT   "RIP3, a novel apoptosis-inducing kinase.";
RL   J. Biol. Chem. 274:16871-16875(1999).
RN   [7]
RP   INTERACTION WITH BNLF1.
RX   MEDLINE=99340272; PubMed=10409763;
RA   Izumi K.M., Cahir McFarland E., Ting A.T., Riley E.A., Seed B.,
RA   Kieff E.D.;
RT   "The Epstein-Barr virus oncoprotein latent membrane protein 1 engages
RT   the tumor necrosis factor receptor-associated proteins TRADD and
RT   receptor-interacting protein (RIP) but does not induce apoptosis or
RT   require RIP for NF-kappaB activation.";
RL   Mol. Cell. Biol. 19:5759-5767(1999).
RN   [8]
RP   INTERACTION WITH IKBKG.
RX   MEDLINE=99128359; PubMed=9927690; DOI=10.1073/pnas.96.3.1042;
RA   Li Y., Kang J., Friedman J., Tarassishin L., Ye J., Kovalenko A.,
RA   Wallach D., Horwitz M.S.;
RT   "Identification of a cell protein (FIP-3) as a modulator of NF-kappaB
RT   activity and as a target of an adenovirus inhibitor of tumor necrosis
RT   factor alpha-induced apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 96:1042-1047(1999).
RN   [9]
```

```
RP   INTERACTION WITH EGFR.
RX   MEDLINE=21153697; PubMed=11116146; DOI=10.1074/jbc.M008458200;
RA   Habib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,
RA   Vartanian T.;
RT   "The epidermal growth factor receptor engages receptor interacting
RT   protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to
RT   activate NF-kappa B. Identification of a novel receptor-tyrosine
RT   kinase signalosome.";
RL   J. Biol. Chem. 276:8865-8874(2001).
RN   [10]
RP   INTERACTION WITH UBCE7IP1.
RX   MEDLINE=21975204; PubMed=11854271; DOI=10.1074/jbc.M108675200;
RA   Chen D., Li X., Zhai Z., Shu H.-B.;
RT   "A novel zinc finger protein interacts with receptor-interacting
RT   protein (RIP) and inhibits tumor necrosis factor (TNF)- and IL1-
RT   induced NF-kappa B activation.";
RL   J. Biol. Chem. 277:15985-15991(2002).
CC   -!- FUNCTION: Promotes apoptosis and activation of NF-kappa-B.
CC       Required for TNFRSF1A mediated activation of NF-kappa-B.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to the death domain of TNFRSF6 and TRADD. Is
CC       recruited by TRADD to TNFRSF1A in a TNF-dependent process. Binds
CC       RIPK3, UBCE7IP1, EGFR, IKBKG, TRAF1, TRAF2 and TRAF3. Interacts
CC       with BNLF1.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- PTM: Proteolytically cleaved by caspase-8 during TNF-induced
CC       apoptosis. Cleavage abolishes NF-kappa-B activation and enhances
CC       pro-apototic signaling through the TRADD-FADD interaction.
CC   -!- PTM: Autophosphorylated on serine and threonine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC   -!- SIMILARITY: Contains 1 death domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U50062; AAC32232.1; -.
DR   EMBL; AL031963; CAD70625.1; -.
DR   EMBL; U25994; AAC50137.1; -.
DR   PIR; T09479; T09479.
DR   HSSP; P41240; 1BYG.
DR   Genew; HGNC:10019; RIPK1.
DR   MIM; 603453; -.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0004871; F:signal transducer activity; IEP.
DR   GO; GO:0006915; P:apoptosis; TAS.
DR   GO; GO:0043123; P:positive regulation of I-kappaB kinase/NF-k. . .; IEP.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00531; Death; 1.
DR   Pfam; PF00069; Pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00005; DEATH; 1.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Apoptosis; ATP-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       17    289       Protein kinase.
FT   NP_BIND      23     31       ATP (By similarity).
FT   BINDING      49     49       ATP (By similarity).
FT   ACT_SITE    138    138       Proton acceptor (By similarity).
FT   DOMAIN      583    669       Death.
FT   DOMAIN      411    414       Poly-Arg.
FT   SITE        324    325       Cleavage (by caspase-8).
FT   MUTAGEN      45     45       K->A: Abolishes kinase activity.
FT   MUTAGEN     324    324       D->K: Abolishes cleavage by caspase-8.
FT   CONFLICT    438    438       V -> A (in Ref. 3).
FT   CONFLICT    514    514       T -> S (in Ref. 4).
SQ   SEQUENCE   671 AA;  75958 MW;  BADC4E7E70456ABE CRC64;

  Query Match             18.8%;  Score 111.5;  DB 1;  Length 671;
  Best Local Similarity   36.4%;  Pred. No. 0.095;
  Matches   28;  Conservative   19;  Mismatches   27;  Indels    3;  Gaps    3;

Qy         23 ICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRN-LTERVRESLRIWKNTEK-ENATVAHL 80
              | :|:|| |:  ||:|  : ::|| |:  | |: | |:| : |: |   |  : |||  |
Db        590 IRENLGKHWKNCARKLGFTQSQIDEIDHDYERDGLKEKVYQMLQKWVMREGIKGATVGKL 649

Qy         81 VGALRSC-QMNLVADLV 96
                ||  | :::|:: |:
Db        650 AQALHQCSRIDLLSSLI 666


Search completed: February 11, 2005, 16:43:05
Job time : 84 secs
```